

**Amendments to the Claims:**

This claim listing will replace all prior versions and listings of claims in the application:

**Claim Listing:**

1. (Currently Amended): A method of classifying a brain tumor comprising the steps of:
  - a) obtaining a sample of cells derived from a brain tumor;
  - b) isolating a polynucleotide gene expression product from at least one informative gene, from one or more cells in said sample, and
  - c) determining a gene expression profile of at least one informative gene by measuring the levels of polynucleotide gene expression products from two or more informative genes from one or more cells derived from a brain tumor, wherein one of said informative genes is M64347, and wherein the gene expression profile is correlated with a specific brain tumor type sub-type.
2. (Cancelled)
3. (Currently Amended): The method of Claim 1 or 2, wherein the brain tumor type is a medulloblastoma or a glioblastoma.  
*C15*
4. (Currently Amended): The method of Claim 3, wherein the medulloblastoma sub-type is classic medulloblastoma or desmoplastic medulloblastoma.
5. (Cancelled)
6. (Cancelled)
7. (Currently Amended): The method of Claim 1, wherein the gene expression product is mRNA.

8. (Original): The method of Claim 7, wherein the gene expression profile is determined utilizing specific hybridization probes.

9. (Original): The method of Claim 7, wherein the gene expression profile is determined utilizing oligonucleotide microarrays.

10. (Canceled)

11. (Canceled)

12. (Currently Amended): A method according to Claim 1, wherein ~~one or more the~~ informative genes ~~is are~~ selected from the group consisting of the genes in Tables 2-6.

13. (Currently Amended): A method according to Claim 1, wherein ~~one or more the~~ informative genes ~~is are~~ selected from the group consisting of the genes in Table 1.

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14. (Currently Amended): A method of predicting the efficacy of treating a brain tumor comprising ~~the steps of:~~

a) ~~obtaining a sample of cells derived from a brain tumor;~~

b) ~~isolating a polynucleotide gene expression product from at least one informative gene from one or more cells in said sample; and~~

c) ~~determining a gene expression profile of at least one informative gene by measuring the levels of polynucleotide gene expression products from two or more informative genes from one or more cells derived from a brain tumor, wherein one of said informative genes is M64347 at, and wherein the gene expression profile is correlated with a treatment outcome, thereby classifying the sample with respect to treatment outcome.~~

15. (Canceled)

16. (Currently Amended) The method of Claim 14 ~~15~~, wherein the brain tumor type is a medulloblastoma or a glioblastoma.

17. (Currently Amended): The method of Claim 16, wherein the medulloblastoma sub-type is classic medulloblastoma or desmoplastic medulloblastoma.

18. (Currently Amended): A method according to Claim 14, wherein the gene expression product is products are mRNA.

19. (Original): A method according to Claim 18, wherein the gene expression profile is determined utilizing specific hybridization probes.

20. (Original): A method according to Claim 18, wherein the gene expression profile is determined utilizing oligonucleotide microarrays.

21. (Canceled)

22. (Canceled)

23. (Original): A method according to Claim 14, wherein the predicted treatment outcome is survival after treatment.

24. (Currently Amended): A method according to Claim 14, wherein one or more the informative genes is are selected from the group consisting of the genes in Table 1.

25. (Currently Amended): A method according to Claim 14, wherein one or more the informative genes is are selected from the group consisting of the genes in Tables 2-6.

26. (Currently Amended): A method of assigning a brain tumor sample to a treatment outcome class for predicting a treatment outcome of a patient from whom a brain tumor sample is obtained, comprising the steps of:

a) determining a weighted vote for one of the classes of one or more informative genes in said sample in accordance with a model built with a weighted voting scheme, wherein the magnitude of each vote depends on the expression level of the gene in said sample and on the degree of correlation of the gene's expression with class distinction; and

b)a) summing the votes to determine the winning class, wherein the winning class is the treatment outcome class to which the brain tumor sample is assigned.

*determining a weighted vote based on gene expression values determined by measuring the levels of polynucleotide gene expression products from two or more informative genes from one or more cells derived from a brain tumor from the patient, wherein one of the informative genes is M64347 at, in accordance with a model built with a weighted voting scheme, wherein each gene for which a polynucleotide gene expression product is measured is assigned a vote, and wherein the magnitude of the vote corresponding to a gene's expression depends on the expression level of the gene and on the degree of correlation of the gene's expression with class distinction; and*

b) summing the votes determined in (a) to determine the winning class, wherein the winning class predicts the treatment outcome of the patient.

27. (Original): The method of Claim 26, wherein the weighted voting scheme is:

$$V_g = a_g (x_g - b_g),$$

wherein  $V_g$  is the weighted vote of the gene,  $g$ ;  $a_g$  is the correlation between gene expression values and class distinction;  $b_g = (\mu_1(g) + \mu_2(g))/2$  is the average of the mean  $\log_{10}$  expression value in a first class and a second class;  $x_g$  is the  $\log_{10}$  gene expression value in the sample to be tested; and wherein a positive  $V$  value indicates a vote for the first class, and a negative  $V$  value indicates a vote for the second class.

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28. (Previously Presented): The method according to Claim 26, wherein the informative genes are selected from the group consisting of the genes in Table 1.

29. (Previously Presented): The method according to Claim 26, wherein the informative genes are selected from the group consisting of the genes in Tables 2-6.

30. (Cancelled)

31. (Currently Amended): A method for evaluating drug candidates for their effectiveness in treating a brain tumor tumors comprising:  
a) obtaining samples of cells derived from a brain tumor;  
b) isolating a polynucleotide gene expression product from at least one informative gene from one or more cells in said samples; and  
c) determining a gene expression profile of at least one informative gene by measuring the levels of polynucleotide gene expression products from two or more informative genes from one or more cells derived from a brain tumor,  
wherein one of said informative genes is M64347 at, before and after treatment with a drug candidate, and comparing the gene expression profile determined before treatment with the gene expression profile determined after treatment,  
wherein a drug candidate which alters the gene expression profile such that the gene expression profile is more similar to a normal gene expression profile after treatment is a drug candidate which may be effective in treating a brain tumor correlated with the effectiveness of the drug candidate in treating brain tumors.

32. (Currently Amended): A method for monitoring the efficacy of a brain tumor treatment comprising:  
a) obtaining samples of cells at various time points derived from a patient being treated determining gene expression profiles at multiple time points during treatment of a patient by measuring the levels of polynucleotide gene expression

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products from two or more informative genes from one or more cells derived from a brain tumor, wherein one of said informative genes is M64347 at; and

- b) determining the polynucleotide expression profile of the samples;
- c) determining classifying the samples for treatment outcome at each time point based on the gene expression profile; and
- d) comparing the treatment outcome class of the samples at various times during treatment, wherein the efficacy of brain tumor treatment is determined.

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33. (Cancelled)

34. (Cancelled)